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nucleotide sequence specific of an organism with a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence and its corresponding capture nucleotide sequence is disclosed. The capture nucleotide sequence is bound to the insoluble solid support at a specific location on an array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm<sup>2</sup>. The location of the signal on the array allows identification or quantification of the organism.

COMMENTS

The specific changes to the abstract are shown on a separate sheet of paper attached hereto entitled **VERSION WITH MARKINGS TO SHOW CHANGES MADE**, which follows the signature page of this amendment. On this paper, the insertions are underlined, while the deletions are struck through.

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: 11/27/01 By: Daniel Hart  
Daniel Hart  
Registration No. 40,490  
620 Newport Center Drive  
Sixteenth Floor  
Newport Beach, CA 92660  
(619) 235-8550

**VERSION WITH MARKINGS TO SHOW CHANGES MADE**

~~The present invention is related to an identification and/or quantification method of a biological (micro)organism or part of it (possibly present in a biological sample) by a detection of a method for identifying or quantifying an organism by a detecting its nucleotide sequence among at least 4 other homologous sequences and comprising the steps of:~~

~~- possibly extracting original nucleotide sequences (1) from the (micro)organism;~~

~~- amplifying or copying with a unique pair of primer(s), at least part of original nucleotide sequences (1) into target nucleotide sequences (2) to be detected;~~

~~- possibly labelling said target nucleotide sequences (2);~~

~~- putting into contact the labelled target nucleotide sequences (2) comprising amplifying nucleic acids from the organism to generate target nucleotide sequences to be detected; contacting the target nucleotide sequences with single stranded capture nucleotide sequences (3) bound by a single predetermined link to an insoluble solid support (4), preferably a non porous solid support;~~

~~- and discriminating the binding of a target nucleotide sequence (2) specific of an organism or part of it by detecting, quantifying and/or recording with a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence (2) and its corresponding capture nucleotide sequence (3);~~

~~- wherein said is disclosed. The capture nucleotide sequence (3) being is bound to the insoluble solid support (4) at a specific location according to an array, said array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm<sup>2</sup> of solid support surface and sequences/cm<sup>2</sup>. The location of the signal on the array allows identification or quantification of the organism.~~

~~wherein the binding between the target nucleotide sequence and its corresponding capture nucleotide sequence forms (will result in) said signal at the expected location, the detection of a single signal allowing a discrimination of the target nucleotide sequence specific of an organism or part of it from homologous nucleotide sequences.~~